AMENDMENT

Amendments in the Specification:

Please replace the sentence before the FIELD OF THE INVENTION with the following amended paragraph:

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a National ~~Phase~~ Stage Application under §371 of International Application Number PCT/AU2004/001783 filed December 17, 2004, which claims priority to Australian Application No. 2003907017 filed December 19, 2003 [[2004]].

Please replace the paragraph of the Abstract with the following amended paragraph:

The invention relates to *Brachyspira pilosicoli* 72 kDa outer-membrane protein (Bpmp-72) and its amino acid and ~~neucleotide~~ nucleotide sequence. The invention also relates to the uses of these sequences in prophylactic (vaccination) and therapeutic treatment of infections with *Brachyspira pilosicoli* (internal spirochaetosis).

Please replace line 3 at page 8 with the following amended line:

Figure 3 Nucleotide sequence of Bpmp-72 (SEQ ID NO:39).

Please replace the paragraph at page 13, line 4, which starts with "Analysis of the Bpmp-72 polynucleotide ..." with the following amended paragraph:

Analysis of the Bpmp-72 polynucleotide sequence revealed a 1009 base pair insert of *B. pilosicoli* genomic DNA (FIG. 3). Sequence analysis of the insert DNA revealed a potential partial ORF of 783 base pair from bases 1 to 783, with a putative ATG start codon and a TAA stop codon. Further cloning and sequencing of the remaining gene revealed the coding sequence of Bpmp-72 to be ~~1,692~~ 1,689 nucleotides in size. A potential Shine-Dalgarno ribosome binding site (AGGAG), and putative -10 (TAATAT) and -35 (TTGAAA) promoter regions were identified upstream from the ATG start codon. The gene sequence encoding the 72 kDa outer-membrane protein was designated outer-membrane protein of 72 kDa molecular weight (Bpmp-72).

Please replace the paragraph at page 13, line 14, which starts with "The translated polypeptide consisted of ..." with the following amended paragraph:

The translated polypeptide consisted of ~~564~~ 563 amino acid (aa) residues with a predicted molecular weight of 62.1 kDa (FIG. 4). The deduced size differed significantly

from those seen in the Western blots of the native Bpmp-72 protein. The difference in molecular weight between the hypothetical coding capacity of Bpmp-72 and the native Bpmp-72 outer-membrane protein is probably due to post-translational modifications such as acylation, methylation, acetylation, phosphorylation and sulphation.

Please replace the paragraph at page 14, line 4, which starts with "Full-length Bpmp-72 ..." with the following amended paragraph:

Full-length Bpmp-72 amino acid sequences provided according to the invention will have about ~~564~~ 563 amino acid (aa) residues and encode a *B. pilosicoli* outer membrane protein. The deduced molecular weight of the protein is 62,081 Da.

Please replace the paragraph at page 58, line 12, which starts with "Sequencing of the AHP1 ..." with the following amended paragraph:

Sequencing of the AHP1 plasmid using the primers listed in Table 2 revealed a 1009 base pair insert of *B. pilosicoli* genomic DNA. Sequence analysis of the insert DNA revealed a potential partial ORF of 783 base pair from bases 1 to 783, with a putative ATG start codon and a TAA stop codon (FIG. 3). Further cloning and sequencing of the remaining gene revealed the coding sequence of Bpmp-72 to be ~~1,692~~ 1,689 nucleotides in size. A potential Shine-Dalgarno ribosome binding site (AGGAG), and putative -10 (TAATAT) and -35 (TTGAAA) promoter regions were identified upstream from the ATG start codon. The gene sequence encoding the 72 kDa outer-membrane protein was designated outer-membrane protein of 72 kDa molecular weight (Bpmp-72).

Please replace the paragraph at page 58, line 22, which starts with "The translated polypeptide consisted of ..." with the following amended paragraph:

The translated polypeptide consisted of ~~564~~ 563 amino acid (aa) residues with a predicted molecular weight of 62.1 kDa. The deduced size differed significantly from those seen in the Western blots of the native Bpmp-72 protein. The difference in molecular weight between the hypothetical coding capacity of Bpmp-72 and the native Bpmp-72 outer-membrane protein is probably due to post-translational modifications such as acylation, methylation, acetylation, phosphorylation and sulphation. Analysis of the amino acid sequence revealed the presence of a 118 residue region at the C-terminus of the translated polypeptide which was homologous to a conserved lysine motif (LysM) domain. This domain is a widespread protein module which was originally identified in enzymes which degrade

bacterial cell walls although it has since been shown to be present in many other bacterial proteins. The LysM domain is one of the most common modules in bacterial cell surface proteins. Other bacterial proteins which possess the LysM domain, such as *Staphlococci* IgG binding proteins and *E. coli* intimin, are involved in bacterial pathogenesis.

Please replace the paragraph at page 59, line 16, which starts with "The Bpmp-72 gene of the six ..." with the following amended paragraph:

The Bpmp-72 gene of the six *B. pilosicoli* strains showed 99.8-100% homology at the nucleotide level (Table 3). All strains posses a ~~1,692~~ 1,689 bp gene which translates into a ~~564~~ 563 amino acid protein. The high level of homology between the different strains of *B. pilosicoli* suggests that Bpmp-72 may be a highly conserved locus within the species.

Please replace the paragraph at page 59, line 21 through page 60, line 2, which starts with "The Bpmp-72 gene of the six ..." with the following amended paragraph:

The Bpmp-72 gene of the six *B. pilosicoli* strains showed 99.3-100% at the amino acid level (Table 4). All strains posses a ~~1,692~~ 1,689 base pair gene which translates into a ~~564~~ 563 amino acid protein. The high level of homology between the different strains of *B. pilosicoli* suggests that Bpmp-72 may be a highly conserved locus within the species.

The attached substitute sheets include changes to the Sequence Listing. These substitute sheets, which include SEQ ID NOs:1-39, replace the original Sequence Listing, which is shown in the published Application under paragraph [0309].

Attachment: Replacement substitute sheets 1-14.